

## SEQUENCE LISTING

- (1) GENERAL INFORMATION:  
(i) NUMBER OF SEQUENCES: 2
- (2) INFORMATION FOR SEQ ID NO. 1:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3884 base pairs  
(B) TYPE: nucleic acid and amino acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULAR TYPE: cDNA  
(vi) ORIGINAL SOURCE:  
(E) ORGANISM: human  
(F) CELLTYPE: chondrocyte  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

1 CAGGTCAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTG 60  
GTCCAGTCTTTGGCTAGTCCGTACCTTGAGGGGAAGCAGTGAGTGGACAAGAACGGGGAC  
a M E L P F V T H L F L P L -

61 GTGTTCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTC 120  
CACAAAGGACTGTCCAGAGACGAGGGGGAAATTGGACCTACTTGTAGTGGGTGCGGATAAG  
a V F L T G L C S P F N L D E H H P R L F -

121 CCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAG 180  
GGTCCCGGTGGTCTTCGACTTAAACCTATGTACAGAAATGTTGTACAACCCCACTGTG  
a P G P P E A E F G Y S V L Q H V G G G Q -

181 CGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT 240  
GCTACCTACGACCACCCGCGGGGGACCCTACCCGGAAGTCCGCTGGCCTCCCCCTGCAA  
a R W M L V G A P W D G P S G D R R G D V -

241 TATCGCTGCCCTGTAGGGGGGGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGAC 300  
ATAGCGACGGGACATCCCCCGGGTGTACGGGGTACACGGTTCGGGTGAATCCACTG  
a Y R C P V G G A H N A P C A K G H L G D -

301 TACCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTA 360  
ATGGTTGACCCTTTAAGTAGAGTAGGACGACACTTATACGTGGACCCCTACAGAGACAAT  
a Y Q L G N S S H P A V N M H L G M S L L -

361 GAGACAGATGGTGTATGGGGGATTTCATGGCCTGTGCCCCCTCTCTGGTCTCGTGTGTTGGC 420  
CTCTGTCTACCACTACCCCTAAGTACCGGACACGGGGAGAGACCAGAGCACGAACACCG  
a E T D G D G G F M A C A P L W S R A C G -

AGCTCTGTTCTTCAGTTCTGGGATATGTGCCCCTGTGGATGCTTCATTCCAGCCTCAGGGA  
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
TCGAGACAGAAAGTCAAGACCCTATACACGGGCACACCTACGAAGTAAGGTCGGAGTCCCT  
a S S V F S S G I C A R V D A S F Q P Q G -  
AGCCTGGCACCCACTGCCCAACGCTGCCCAACATACATGGATGTTGTTCATTGTCTTGGAT  
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
TCGGACCGTGGGTGACGGGTTGCGACGGGTTGTATGTACCTACAACAGTAACAGAACCTA  
a S L A P T A Q R C P T Y M D V V I V L D -  
GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGACCTTCCTACGAAGACTGGTAGGG  
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
CCGAGGTTGTCGTAGATGGGGACCAGACTTCAAGTCTGGAAGGATGCTTCTGACCATCCC  
a G S N S I Y P W S E V Q T F L R R L V G -  
AAACTGTTTATTGACCCAGAACAGATACAGGTGGGACTGGTACAGTATGGGGAGAGCCCT  
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660  
TTTGACAAATAACTGGGTCTTGTCTATGTCCACCCTGACCATGTACATCCCTCTCGGGA  
a K L F I D P E Q I Q V G L V Q Y G E S P -  
GTACATGAGTGGTCCCTGGGAGATTTCGAACGAAGGAAGAAGTGGTGAGAGCAGCAAAG  
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720  
CATGTACTCACCAGGGACCCTCTAAAGCTTGCTTCCTTCTTCACCACTCTCGTCGTTTC  
a V H E W S L G D F R T K E E V V R A A K -  
AACCTCAGTCGGCGGGAGGGACGAGAAACAAGACTGCCCAAGCAATAATGGTGGCCTGC  
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780  
TTGGAGTCAGCCGCCCTCCCTGCTCTTGTCTCTGACGGGTTGCTTATTACCACCGGACG  
a N L S R R E G R E T K T A Q A I M V A C -  
ACAGAAGGGTTCAGTCAGTCCCATGGGGGCCGACCCGAGGCTGCCAGGCTACTGGTGGTT  
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
TGTCTTCCCAAGTCAGTCAGGTACCCCGGCTGGGCTCCGACGGTCCGATGACCACCAA  
a T E G F S Q S H G G R P E A A R L L V V -  
GTCACTGATGGAGAGTCCCATGATGGAGAGGAGCTTCCTGCAGCACTAAAGGCCTGTGAG  
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900  
CAGTGA CTACCTCTCAGGGTACTACCTCTCCTCGAAGGACGTCGTGATTCCGGACACTC  
a V T D G E S H D G E E L P A A L K A C E -  
GCTGGAAGAGTGACACGCTATGGGATTGCAGTCCTTGGTCACTACCTCCGGCGGCAGCGA  
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960  
CGACCTTCTCACTGTGCGATACCCTAACGTCAGGAACCAAGTATGGAGGCCCGCTCGCT  
a A G R V T R Y G I A V L G H Y L R R Q R -  
GATCCCAGCTCTTTCTGAGAGAAATTAGAACTATTGCCAGTGATCAGATGAGCGATTTC  
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
CTAGGGTCGAGAAAGGACTCTCTTTAATCTTGATAACGGTCACTAGGTCTACTCGCTAAG  
a D P S S F L R E I R T I A S D P D E R F -  
TTCTTCAATGTCACAGATGAGGCTGCTCTGACTGACATTGTGGATGCACTAGGAGATCGG  
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
AAGAAGTTACAGTGTCTACTCCGACGAGACTGACTGTAACACCTACGTGATCCTCTAGCC  
a F F N V T D E A A L T D I V D A L G D R -

ATTTTGGCCTTGAAGGGTCCCATGCAGAAAACGAAAGCTCCTTTGGGCTGGAAATGTCT  
1081 -----+-----+-----+-----+-----+ 1140  
TAAAAACCGAACTTCCCAGGTACGTCTTTTGCTTTCGAGGAAACCCGACCTTTACAGA  
a I F G L E G S H A E N E S S F G L E M S -  
CAGATTGGTTTCTCCACTCATCGGCTAAAGGATGGGATTCTTTTGGGATGGTGGGGGCC  
1141 -----+-----+-----+-----+-----+ 1200  
GTCTAACCAAGAGGTGAGTAGCCGATTTCCTACCCTAAGAAAAACCCTACCACCCCCGG  
a Q I G F S T H R L K D G I L F G M V G A -  
TATGACTGGGGAGGCTCTGTGCTATGGCTTGAAGGAGGCCACCGCCTTTTCCCCCACGA  
1201 -----+-----+-----+-----+-----+ 1260  
ATACTGACCCCTCCGAGACACGATACCGAACTTCCTCCGGTGGCGGAAAAGGGGGGTGCT  
a Y D W G G S V L W L E G G H R L F P P R -  
ATGGCACTGGAAGACGAGTTCCCTCCCTGCACTGCAGAACCATGCAGCCTACCTGGGTTAC  
1261 -----+-----+-----+-----+-----+ 1320  
TACCGTGACCTTCTGCTCAAGGGGGGACGTGACGTCTTGGTACGTGGATGGACCCAATG  
a M A L E D E F P P A L Q N H A A Y L G Y -  
TCTGTTTCTTCCATGCTTTTTCGGGGTGGACGCCGCTGTTTCTCTCTGGGGCTCCTCGA  
1321 -----+-----+-----+-----+-----+ 1380  
AGACAAAGAAGGTACGAAAACGCCCACTGCGGCGGACAAAGAGAGACCCCGAGGAGCT  
a S V S S M L L R G G R R L F L S G A P R -  
TTTAGACATCGAGGAAAAGTCATCGCCTTCCAGCTTAAGAAAGATGGGGCTGTGAGGGTT  
1381 -----+-----+-----+-----+-----+ 1440  
AAATCTGTAGCTCCTTTTCAGTAGCGGAAGGTGAATTCTTTCTACCCCGACACTCCCAA  
a F R H R G K V I A F Q L K K D G A V R V -  
GCCCAGAGCCTCCAGGGGGAGCAGATTGGTTCATACTTTGGCAGTGAGCTCTGCCCATTG  
1441 -----+-----+-----+-----+-----+ 1500  
CGGGTCTCGGAGGTCCCCCTCGTCTAACCAAGTATGAACCGTCACTCGAGACGGGTAAC  
a A Q S L Q G E Q I G S Y F G S E L C P L -  
GATACAGATAGGGATGGAACAACTGATGTCTTACTTGTGGCTGCCCCCATGTTCTGGGA  
1501 -----+-----+-----+-----+-----+ 1560  
CTATGTCTATCCCTACCTTGTGACTACAGAATGAACACCGACGGGGGTACAAGGACCCT  
a D T D R D G T T D V L L V A A P M F L G -  
CCCCAGAACAAGGAAACAGGACGTGTTTATGTGTATCTGGTAGGCCAGCAGTCCTTGCTG  
1561 -----+-----+-----+-----+-----+ 1620  
GGGGTCTTGTTCCTTTGTCTGCACAAATACATAGACCATCGGGTCGTACAGGAACGAC  
a P Q N K E T G R V Y V Y L V G Q Q S L L -  
ACCCTCCAAGGAACACTTCAGCCAGAACCCCCCAGGATGCTCGGTTTGGCTTTGCCATG  
1621 -----+-----+-----+-----+-----+ 1680  
TGGGAGGTTCTTGTGAAGTCGGTCTTGGGGGGTCTACGAGCCAAACCGAAACGGTAC  
a T L Q G T L Q P E P P Q D A R F G F A M -  
GGAGCTCTTCTGATCTGAACCAAGATGGTTTGTGCTGATGTGGCTGTGGGGGCGCCTCTG  
1681 -----+-----+-----+-----+-----+ 1740  
CCTCGAGAAGGACTAGACTTGGTTCTACAAAACGACTACACCGACACCCCGCGGAGAC  
a G A L P D L N Q D G F A D V A V G A P L -

GAAGATGGGCACCAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCCC  
1741 -----+-----+-----+-----+-----+ 1800  
CTTCTACCCGTGGTCCCTCGTGACATGGACATGGTACCTTGGGTCTCACCTCAGTCCGGG

a E D G H Q G A L Y L Y H G T Q S G V R P -

CATCCTGCCCAGAGGATTGCTGCTGCCTCCATGCCACATGCCCTCAGCTACTTTGGCCGA  
1801 -----+-----+-----+-----+-----+ 1860  
GTAGGAAGGGTCTCCTAACGACGACGGAGGTACGGTGTACGGGAGTCGATGAAACCGGCT

a H P A Q R I A A A S M P H A L S Y F G R -

AGTGTGGATGGTCCGCTAGATCTGGATGGAGATGATCTGGTTCGATGTGGCTGTGGGTGCC  
1861 -----+-----+-----+-----+-----+ 1920  
TCACACCTACCAGCCGATCTAGACCTACCTCTACTAGACCAGCTACACCGACACCCACGG

a S V D G R L D L D G D D L V D V A V G A -

CAGGGGGCAGCCATCCTGCTCAGCTCCCGGCCATTGTCCATCTGACCCCATCACTGGAG  
1921 -----+-----+-----+-----+-----+ 1980  
GTCCCCCGTCGGTAGGACGAGTCGAGGGCCGGGTAACAGGTAGACTGGGGTAGTGACCTC

a Q G A A I L L S S R P I V H L T P S L E -

GTGACCCACAGGCCATCAGTGTGGTTCAGAGGGACTGTAGGCGGCGAGGCCAAGAAGCA  
1981 -----+-----+-----+-----+-----+ 2040  
CACTGGGGTGTCCGGTAGTCACACCAAGTCTCCCTGACATCCGCCGCTCCGGTTCTTCGT

a V T P Q A I S V V Q R D C R R R G Q E A -

GTCTGTCTGACTGCAGCCCTTTGCTTCCAAGTGACCTCCCGTACTCCTGGTCGCTGGGAT  
2041 -----+-----+-----+-----+-----+ 2100  
CAGACAGACTGACGTCGGGAAACGAAGGTTCACTGGAGGGCATGAGGACCAGCGACCCCTA

a V C L T A A L C F Q V T S R T P G R W D -

CACCAATTCTACATGAGGTTACCCCATCACTGGATGAATGGACTGCTGGGGCACGTGCA  
2101 -----+-----+-----+-----+-----+ 2160  
GTGGTTAAGATGTACTCCAAGTGGCGTAGTGACCTACTTACCTGACGACCCCGTGACGT

a H Q F Y M R F T A S L D E W T A G A R A -

GCATTTGATGGCTCTGGCCAGAGGTTGTCCCTCGGAGGCTCCGGCTCAGTGTGGGGAAT  
2161 -----+-----+-----+-----+-----+ 2220  
CGTAAACTACCGAGACCGGTCTCCAACAGGGAGCCTCCGAGGCCGAGTCACACCCCTTA

a A F D G S G Q R L S P R R L R L S V G N -

GTCACTTGTGAGCAGCTACACTTCCATGTGCTGGATACATCAGATTACCTCCGGCCAGTG  
2221 -----+-----+-----+-----+-----+ 2280  
CAGTGAACACTCGTCGATGTGAAGGTACACGACCTATGTAGTCTAATGGAGGCCGGTCAC

a V T C E Q L H F H V L D T S D Y L R P V -

GCCTTGACTGTGACCTTTGCCTTGGACAATACTACAAAGCCAGGGCCTGTGCTGAATGAG  
2281 -----+-----+-----+-----+-----+ 2340  
CGGAACTGACACTGGAACCGAACCTGTTATGATGTTTCGGTCCCGGACACGACTTACTC

a A L T V T F A L D N T T K P G P V L N E -

GGCTCACCCACCTCTATACAAAAGCTGGTCCCCTTCTCAAAGGATTGTGGCCCTGACAAT  
2341 -----+-----+-----+-----+-----+ 2400  
CCGAGTGGGTGGAGATATGTTTTCGACCAGGGGAAGAGTTTCCTAACACCGGGACTGTTA

a G S P T S I Q K L V P F S K D C G P D N -

GAATGTGTCACAGACCTGGTGCCTCAAGTGAATATGGACATCAGAGGCTCCAGGAAGGCC  
2401 -----+-----+-----+-----+-----+ 2460  
CTTACACAGTGTCTGGACCACGAAGTTCACCTTATACCTGTAGTCTCCGAGGTCCTTCCGG  
a E C V T D L V L Q V N M D I R G S R K A -  
CCATTTGTGTTTCGAGGTGGCCGGCGGAAAGTGCTGGTATCTACAACCTCTGGAGAACAGA  
2461 -----+-----+-----+-----+-----+ 2520  
GGTAAACACCAAGCTCCACCGGCCCTTTACGACCATAGATGTTGAGACCTCTTGTCT  
a P F V V R G G R R K V L V S T T L E N R -  
AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTTCTCTAGAAACCTCCACCTGGCC  
2521 -----+-----+-----+-----+-----+ 2580  
TTCCTTTTACGAATGTATGCTCGGACTCATAGTAGAAGAGATCTTTGGAGGTGGACCGG  
a K E N A Y N T S L S I I F S R N L H L A -  
AGTCTCACTCCTCAGAGAGAGAGCCCAATAAAGGTGGAATGTGCCGCCCTTCTGCTCAT  
2581 -----+-----+-----+-----+-----+ 2640  
TCAGAGTGAGGAGTCTCTCTCTCGGGTTATTTCCACCTTACACGGCGGGGAAGACGAGTA  
a S L T P Q R E S P I K V E C A A P S A H -  
GCCC GGCTCTGCAGTGTGGGGCATCCTGTCTTCCAGACTGGAGCCAAGGTGACCTTTCTG  
2641 -----+-----+-----+-----+-----+ 2700  
CGGGCCGAGACGTCACACCCCGTAGCAGAGAAGGTCTGACCTCGGTTCCACTGGAAGAC  
a A R L C S V G H P V F Q T G A K V T F L -  
CTAGAGTTTGAGTTTAGCTGCTCCTCTCTCTGAGCCAGGTCTTTGGGAAGCTGACTGCC  
2701 -----+-----+-----+-----+-----+ 2760  
GATCTCAAACCTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCCTTCGACTGACGG  
a L E F E F S C S S L L S Q V F G K L T A -  
AGCAGTGACAGCCTGGAGAGAAATGGCACCCTTCAAGAAAACACAGCCAGACCTCAGCC  
2761 -----+-----+-----+-----+-----+ 2820  
TCGTCACTGTCTGGACCTCTCTTACCGTGGGAAGTCTTTTGTGTCGGGTCTGGAGTCGG  
a S S D S L E R N G T L Q E N T A Q T S A -  
TACATCCAATATGAGCCCCACCTCCTGTTCTCTAGTGAGTCTACCCTGCACCGCTATGAG  
2821 -----+-----+-----+-----+-----+ 2880  
ATGTAGGTTATACTCGGGGTGGAGGACAAGAGATCACTCAGATGGGACGTGGCGATACTC  
a Y I Q Y E P H L L F S S E S T L H R Y E -  
GTTCACCCATATGGGACCCTCCCAGTGGGTCTGGCCAGAAATCAAACCACTCTCAGG  
2881 -----+-----+-----+-----+-----+ 2940  
CAAGTGGGTATACCCTGGGAGGGTCACCCAGGACCGGTCTTAAGTTTTGGTGAGAGTCC  
a V H P Y G T L P V G P G P E F K T T L R -  
GTTCAGAACCTAGGCTGCTATGTGGTCAGTGGCCTCATCATCTCAGCCCTCCTTCCAGCT  
2941 -----+-----+-----+-----+-----+ 3000  
CAAGTCTTGATCCGACGATACACAGTCACCGAGTAGTAGAGTCGGGAGGAAGGTCTGA  
a V Q N L G C Y V V S G L I I S A L L P A -  
GTGGCCCATGGGGGCAATTACTTCTATCACTGTCTCAAGTCATCACTAAACATGCAAGC  
3001 -----+-----+-----+-----+-----+ 3060  
CACCGGTACCCCCGTTAATGAAGGATAGTGACAGAGTTCAGTAGTGATTCTTACGTTCCG  
a V A H G G N Y F L S L S Q V I T N N A S -

3061 TGCATAGTGCAGAACCTGACTGAACCCCCAGGCCACCTGTGCATCCAGAGGAGCTTCAA  
-----+-----+-----+-----+-----+ 3120  
ACGTATCACGTCTTGGACTGACTTGGGGGTCCGGGTGGACACGTAGGTCTCCTCGAAGTT

a C I V Q N L T E P P G P P V H P E E L Q -

3121 CACACAAACAGACTGAATGGGAGCAATACTCAGTGTGAGGTGGTGGAGGTGCCACCTTGGG  
-----+-----+-----+-----+-----+ 3180  
GTGTGTTTGTCTGACTTACCCTCGTTATGAGTCACAGTCCACCACTCCACGGTGAACCC

a H T N R L N G S N T Q C Q V V R C H L G -

3181 CAGCTGGCAAAGGGGACTGAGGTCTCTGTTGGACTATTGAGGCTGGTTCACAATGAATTT  
-----+-----+-----+-----+-----+ 3240  
GTCGACCGTTTCCCCTGACTCCAGAGACAACCTGATAACTCCGACCAAGTGTTACTTAAA

a Q L A K G T E V S V G L L R L V H N E F -

3241 TTCCGAAGAGCCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTTTGAGCTGGGAACCGAA  
-----+-----+-----+-----+-----+ 3300  
AAGGCTTCTCGGTTCAAGTTCAAGGACTGCCACCACTCGTGGAAACTCGACCTTGGCTT

a F R R A K F K S L T V V S T F E L G T E -

3301 GAGGGCAGTGTCTACAGCTGACTGAAGCCTCCCGTTGGAGTGAGAGCCTCTTGGAGGTG  
-----+-----+-----+-----+-----+ 3360  
CTCCCGTCACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTCTCGGAGAACCTCCAC

a E G S V L Q L T E A S R W S E S L L E V -

3361 GTTCAGACCCGGCCTATCCTCATCTCCTGTGGATCCTCATAGGCAGTGTCTGGGAGGG  
-----+-----+-----+-----+-----+ 3420  
CAAGTCTGGGCCGGATAGGAGTAGAGGGACACCTAGGAGTATCCGTCACAGGACCCCTCC

a V Q T R P I L I S L W I L I G S V L G G -

3421 TTGCTCCTGCTTGCTCTCCTTGTCTTCTGCTGTGGAAGCTTGGCTTCTTTGCCATAAG  
-----+-----+-----+-----+-----+ 3480  
AACGAGGACGAACGAGAGGAACAGAAGACGGACACCTTCGAACCGAAGAAACGGGTATTC

a L L L L A L L V F C L W K L G F F A H K -

3481 AAAATCCCTGAGGAAGAAAAAGAGAAGAGAAGTTGGAGCAATGAATGTAGAATAAGGGT  
-----+-----+-----+-----+-----+ 3540  
TTTAGGGGACTCCTTCTTTTCTCTTCTCTTCAACCTCGTTACTTACATCTTATTCCCA

a K I P E E E K R E E K L E Q

3541 CTAGAAAGTCCTCCCTGGCAGCTTTCTTCAAGAGACTTGCATAAAAGCAGAGGTTTGGGG  
-----+-----+-----+-----+-----+ 3600  
GATCTTTCAGGAGGGACCGTCGAAAGAAGTTCTCTGAACGTATTTTCGTCTCCAAACCCC

3601 GCTCAGATGGGACAAGAAGCCGCTCTGGACTATCTCCCAGACCAGCAGCCTGACTTGA  
-----+-----+-----+-----+-----+ 3660  
CGAGTCTACCCTGTTCTTCGGCGGAGACCTGATAGAGGGCTCTGGTCGTCGGACTGAACT

3661 CTTTGTAGTCCTAGGGATGCTGCTGGCTAGAGATGAGGCTTACCTCAGACAAGAAGAGC  
-----+-----+-----+-----+-----+ 3720  
GAAAACTCAGGATCCCTACGACGACCGATCTCTACTCCGAAATGGAGTCTGTTCTTCTCG

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3721 TGGCACCAAACTAGCCATGCTCCCACCCCTCTGCTTCCCTCCTCCTCGTGATCCTGGTTC  
-----+-----+-----+-----+-----+-----+ 3780  
ACCGTGGTTTTGATCGGTACGAGGGTGGGAGACGAAGGGAGGAGGAGCACTAGGACCAAG

3781 CATAGCCAACACTGGGGCTTTTGTGTTGGGGTCCTTTTATCCCAGGAATCAATAATTTT  
-----+-----+-----+-----+-----+-----+ 3840  
GTATCGGTTGTGACCCCGAAACAAACCCAGGAAAATAGGGGTCCTTAGTTATTAAAAA

3841 TTGCCTAGGAAAAAAAAAAGCGGCCGCGAATTCGATATCAAGCT  
-----+-----+-----+-----+-----+-----+ 3884  
AACGGATCCTTTTTTTTTTCGCGGCCGCTTAAGCTATAGTTCGA

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## (2) INFORMATION FOR SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3779 base pairs
- (B) TYPE: nucleic acid and amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (E)

## (i) MOLECULAR TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) CELLTYPE: chondrocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

CAGGTCAGAAACCGATCAGGCATGGAACCTCCCTTCGTCACCTGTTCTTGCCCTG  
1 -----+-----+-----+-----+-----+ 60  
GTCCAGTCTTTGGCTAGTCCGTACTTGAGGGGAAGCAGTGAGTGGACAAGAACGGGGAC  
M E L P F V T H L F L P L -  
GTGTTCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTC  
61 -----+-----+-----+-----+-----+ 120  
CACAAAGGACTGTCCAGAGACGAGGGGGAAATTGGACCTACTTGTAGTGGGTGCGGATAAG  
a V F L T G L C S P F N L D E H H P R L F -  
CCAGGGCCACCAGAAGCTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAG  
121 -----+-----+-----+-----+-----+ 180  
GGTCCCGGTGGTCTTCGACTTAAACCTATGTACAGAAATGTTGTACAACCCCCACCTGTC  
a P G P P E A E F G Y S V L Q H V G G G Q -  
CGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCTTCAGGCGACCGGAGGGGGGACGTT  
181 -----+-----+-----+-----+-----+ 240  
GCTACCTACGACCACCCGCGGGGACCTACCCGGAAGTCCGCTGGCCTCCCCCTGCA  
a R W M L V G A P W D G P S G D R R G D V -  
TATCGCTGCCCTGTAGGGGGGGCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGAC  
241 -----+-----+-----+-----+-----+ 300  
ATAGCGACGGGACATCCCCCGGGTGTACGGGGTACAGGTTCCCGGTGAATCCACTG  
a Y R C P V G G A H N A P C A K G H L G D -  
TACCAACTGGGAAATTCATCTCATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTA  
301 -----+-----+-----+-----+-----+ 360  
ATGGTTGACCCTTTAAGTAGAGTAGGACGACACTTATACGTGGACCCCTACAGAGACAAT  
a Y Q L G N S S H P A V N M H L G M S L L -  
GAGACAGATGGTGTATGGGGGATTGATGGCCTGTGCCCTCTCTGGTCTCGTGCTGTGGC  
361 -----+-----+-----+-----+-----+ 420  
CTCTGTCTACCACTACCCCTAAGTACCGGACACGGGGAGAGACCAGACGACGAACCCG  
a E T D G D G G F M A C A P L W S R A C G -  
AGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGA  
421 -----+-----+-----+-----+-----+ 480  
TCGAGACAGAAGTCAAGACCCTATACACGGGCACACCTACGAAGTAAGGTGGGAGTCCCT



44

a S S V F S S G I C A R V D A S F Q P Q G -  
AGCCTGGCACCCACTGCCAACGCTGCCAACATACATGGATGTTGTCTATTGTCTTGGAT  
481 -----+-----+-----+-----+-----+ 540  
TCGGACCGTGGGTGACGGGTTGCGACGGGTTGTATGTACCTACAACAGTAACAGAACCTA

a S L A P T A Q R C P T Y M D V V I V L D -  
GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGACCTTCCTACGAAGACTGGTAGGG  
541 -----+-----+-----+-----+-----+ 600  
CCGAGGTTGTCTAGATGGGGACCAGACTTCAAGTCTGGAAGGATGCTTCTGACCATCCC

a G S N S I Y P W S E V Q T F L R R L V G -  
AAACTGTTTATTGACCCAGAACAGATACAGGTGGGACTGGTACAGTATGGGGAGAGCCCT  
601 -----+-----+-----+-----+-----+ 660  
TTTGACAAATAACTGGGTCTTGTCTATGTCCACCCTGACCATGTCATACCCCTCTCGGGA

a K L F I D P E Q I Q V G L V Q Y G E S P -  
GTACATGAGTGGTCCCTGGGAGATTTCCGAACGAAGGAAGAAGTGGTGAGAGCAGCAAAG  
661 -----+-----+-----+-----+-----+ 720  
CATGTACTCACCAGGGACCCTCTAAAGGCTTGCTTCCTTCTTCACTACTCTCGTCGTTTC

a V H E W S L G D F R T K E E V V R A A K -  
AACCTCAGTCGGCGGGAGGGACGAGAAACAAAGACTGCCCAAGCAATAATGGTGGCCTGC  
721 -----+-----+-----+-----+-----+ 780  
TTGGAGTCAGCCGCCCTCCCTGCTCTTTGTTTCTGACGGGTTCGTTATTACCACGGGACG

a N L S R R E G R E T K T A Q A I M V A C -  
ACAGAAGGGTTCAGTCAGTCCCATGGGGGCCGACCCGAGGCTGCCAGGCTACTGGTGGTT  
781 -----+-----+-----+-----+-----+ 840  
TGTCTTCCCAAGTCAGTCAGGGTACCCCGGCTGGGCTCCGACGGTCCGATGACCACCAA

a T E G F S Q S H G G R P E A A R L L V V -  
GTCAGTATGGAGAGTCCCATGATGGAGAGGAGCTTCTGCAAGCACTAAAGGCCTGTGAG  
841 -----+-----+-----+-----+-----+ 900  
CAGTGACTACCTCTCAGGGTACTACCTCTCCTCGAAGGACGTCCTGATTTCCGGACACTC

a V T D G E S H D G E E L P A A L K A C E -  
GCTGGAAGAGTGACACGCTATGGGATTGCAGTCTTGGTCACTACCTCCGGCGGCAGCGA  
901 -----+-----+-----+-----+-----+ 960  
CGACCTTCTCACTGTGCGATACCCTAACGTCAGGAACCAGTGATGGAGGCCGCCGTCGCT

a A G R V T R Y G I A V L G H Y L R R Q R -  
GATCCCAGCTCTTCTCTGAGAGAAATTAGAACTATTGCCAGTGATCCAGATGAGCGATT  
961 -----+-----+-----+-----+-----+ 1020  
CTAGGGTCGAGAAAGGACTCTCTTTAATCTTGATAACGGTCACTAGGTCTACTCGCTAAG

a D P S S F L R E I R T I A S D P D E R F -  
TTCTTCAATGTCACAGATGAGGCTGCTCTGACTGACATTGTGGATGCACTAGGAGATCGG  
1021 -----+-----+-----+-----+-----+ 1080  
AAGAAGTTACAGTGTCTACTCCGACGAGACTGACTGTAACACCTACGTGATCTCTAGCC

a F F N V T D E A A L T D I V D A L G D R -  
ATTTTGGCCTTGAAGGGTCCCATGCAGAAAACGAAAGCTCCTTTGGGCTGGAAATGTCT  
1081 -----+-----+-----+-----+-----+ 1140  
TAAAAACCGGAACCTCCAGGGTACGTCTTTTGCTTTCGAGGAAACCCGACCTTACAGA

45

a I F G L E G S H A E N E S S F G L E M S -  
CAGATTGGTTTCTCCACTCATCGGCTAAAGGATGGGATTCTTTTTGGGATGGTGGGGGCC  
1141 -----+-----+-----+-----+-----+-----+-----+ 1200  
GTCTAACCAGAGGTGAGTAGCCGATTTCTACCTAAGAAAACCTACCACCCCGG

a Q I G F S T H R L K D G I L F G M V G A -  
TATGACTGGGAGGCTCTGTGCTATGGCTTGAAGGAGGCCACCGCCTTTTCCCCCACGA  
1201 -----+-----+-----+-----+-----+-----+-----+ 1260  
ATACTGACCCCTCCGAGACACGATACCGAACTTCTCCGGTGGCGGAAAAGGGGGTGTCT

a Y D W G G S V L W L E G G H R L F P P R -  
ATGGCACTGGAAGACGAGTTCCCCCTGCACTGCAGAACCATGCAGCCTACCTGGGTTAC  
1261 -----+-----+-----+-----+-----+-----+-----+ 1320  
TACCGTGACCTTCTGCTCAAGGGGGACGTGACGTCTTGGTACGTCGGATGGACCCAATG

a M A L E D E F P P A L Q N H A A Y L G Y -  
TCTGTTTCTTCCATGCTTTTGGGGGTGGACGCCGCTGTTTCTCTCTGGGGCTCCTCGA  
1321 -----+-----+-----+-----+-----+-----+-----+ 1380  
AGACAAAGAGGTACGAAACGCCCCACCTGCGGCGGACAAAGAGAGACCCCGAGGAGCT

a S V S S M L L R G G R R L F L S G A P R -  
TTTAGACATCGAGGAAAAGTCATCGCCTTCCAGCTTAAGAAAGATGGGGCTGTGAGGGTT  
1381 -----+-----+-----+-----+-----+-----+-----+ 1440  
AAATCTGTAGCTCCTTTTCAGTAGCGGAAGGTGGAATTCTTTCTACCCCGACACTCCCAA

a F R H R G K V I A F Q L K K D G A V R V -  
GCCCAGAGCCTCCAGGGGGAGCAGATTGGTTCATACTTTGGCAGTGAGCTCTGCCCATTG  
1441 -----+-----+-----+-----+-----+-----+-----+ 1500  
CGGGTCTCGGAGGTCCCCCTCGTCTAACCAAGTATGAAACCGTCACTCGAGACGGGTAAC

a A Q S L Q G E Q I G S Y F G S E L C P L -  
GATACAGATAGGGATGGAACAACTGATGTCTTACTTGTGGCTGCCCCCATGTTCTGGGA  
1501 -----+-----+-----+-----+-----+-----+-----+ 1560  
CTATGTCTATCCCTACCTTGTGACTACAGATGAACACCGACGGGGGTACAAGGACCTT

a D T D R D G T T D V L L V A A P M F L G -  
CCCCAGAACAAGGAAACAGGACGTGTTTATGTGTATCTGGTAGGCCAGCAGTCCTTGCTG  
1561 -----+-----+-----+-----+-----+-----+-----+ 1620  
GGGGTCTTGTTCCTTTGTCTGACAAATACACATAGACCATCCGGTCTGAGGAACGAC

a P Q N K E T G R V Y V Y L V G Q Q S L L -  
ACCCTCCAAGGAACACTTCAGCCAGAACCCCCCAGGATGCTCGGTTTGGCTTTGCCATG  
1621 -----+-----+-----+-----+-----+-----+-----+ 1680  
TGGGAGGTTCTTGTGAAGTCGGTCTTGGGGGGTCTACGAGCCAAACCGAAACGGTAC

a T L Q G T L Q P E P P Q D A R F G F A M -  
GGAGCTCTTCTGATCTGAACCAAGATGGTTTTGCTGATCTGGCTGTGGGGGCGCCTCTG  
1681 -----+-----+-----+-----+-----+-----+-----+ 1740  
CCTCGAGAAGGACTAGACTTGGTTCTACCAAACGACTACACCGACACCCCGCGGAGAC

a G A L P D L N Q D G F A D V A V G A P L -  
GAAGATGGGCACCAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCCC  
1741 -----+-----+-----+-----+-----+-----+-----+ 1800  
CTTCTACCCGTGGTCCCTCGTGACATGGACATGGTACCTTGGGTCTCACCTCAGTCCGGG

GAGGTTTCTTCCATGCTTTTGGGGGTGGACGCCGCTGTTTCTCTCTGGGGCTCCTCGA

46

a E D G H Q G A L Y L Y H G T Q S G V R P -  
CATCCTGCCCAGAGGATTGCTGCTGCCATGCCACATGCCCTCAGCTACTTTGGCCGA  
1801 -----+-----+-----+-----+ 1860  
GTAGGACGGGTCTCCTAACGACGACGGAGGTACGGTGTACGGGAGTCGATGAAACCGGCT

a H P A Q R I A A A S M P H A L S Y F G R -  
AGTGTGGATGGTGGCTAGATCTGGATGGAGATGATCTGGTTCGATGTGGCTGTGGGTGCC  
1861 -----+-----+-----+-----+ 1920  
TCACACCTACCAGCCGATCTAGACCTACCTCTACTAGACCAGCTACACCGACACCCACGG

a S V D G R L D L D G D D L V D V A V G A -  
CAGGGGGCAGCCATCCTGCTCAGTCCCAGGCCATTGTCCATCTGACCCCATCACTGGAG  
1921 -----+-----+-----+-----+ 1980  
GTCCCCCGTCGGTAGGACGAGTCGAGGGCCGGTAACAGGTAGACTGGGGTAGTGACCTC

a Q G A A I L L S S R P I V H L T P S L E -  
GTGACCCACAGGCCATCAGTGTGGTTCAGAGGGACTGTAGGCGGCGAGGCCAAGAAGCA  
1981 -----+-----+-----+-----+ 2040  
CACTGGGGTGTCCGGTAGTCACACCAAGTCTCCCTGACATCCGCCGCTCCGGTTCTTCGT

a V T P Q A I S V V Q R D C R R R G Q E A -  
GTCTGTCTGACTGCAGCCCTTTGCTTCAAGTGACCTCCCGTACTCCTGGTCGCTGGGAT  
2041 -----+-----+-----+-----+ 2100  
CAGACAGACTGACGTCGGGAAACGAAGGTTCACTGGAGGGCATGAGGACCAGCGACCCTA

a V C L T A A L C F Q V T S R T P G R W D -  
CACCAATTCTACATGAGGTTACCGCATCACTGGATGAATGGACTGCTGGGGCACGTGCA  
2101 -----+-----+-----+-----+ 2160  
GTGGTTAAGATGTACTCCAAGTGGCGTAGTGACCTACTTACCTGACGACCCCGTCACGT

a H Q F Y M R F T A S L D E W T A G A R A -  
GCATTTGATGGCTCTGGCCAGAGGTTGTCCCTCGGAGGCTCCGGCTCAGTGTGGGGAAT  
2161 -----+-----+-----+-----+ 2220  
CGTAAACTACCGAGACCGGTCTCCAACAGGGGAGCTCCGAGGCCGAGTCACACCCCTTA

a A F D G S G Q R L S P R R L R L S V G N -  
GTCACTTGTGAGCAGCTACACTTCCATGTGCTGGATACATCAGATTACCTCCGGCCAGTG  
2221 -----+-----+-----+-----+ 2280  
CAGTGAACACTCGTCGATGTGAAGGTACACGACCTATGTAGTCTAATGGAGGCCGGTCAC

a V T C E Q L H F H V L D T S D Y L R P V -  
GCCTTGACTGTGACCTTTGCCTTGACAATACTACAAAGCCAGGGCCTGTGCTGAATGAG  
2281 -----+-----+-----+-----+ 2340  
CGGAAGTGAAGTGGAAACGGAACCTGTTATGATGTTTCGGTCCCGGACACGACTTACTC

a A L T V T F A L D N T T K P G P V L N E -  
GGCTCACCCACCTCTATACAAAAGCTGGTCCCCTTCTCAAAGGATTGTGGCCCTGACAAT  
2341 -----+-----+-----+-----+ 2400  
CCGAGTGGGTGGAGATATGTTTCGACCAGGGGAAGAGTTTCCTAACACCGGACTGTTA

a G S P T S I Q K L V P F S K D C G P D N -  
GAATGTGTCACAGACCTGGTGCTTCAAGTGAATATGGACATCAGAGCTCCAGGAAGGCC  
2401 -----+-----+-----+-----+ 2460  
CTTACACAGTGTCTGGACCACGAAGTCACTTATACCTGTAGTCTCCGAGGTCCTCCGG

a E C V T D L V L Q V N M D I R G S R K A -  
2461 CCATTTGTGGTTCGAGGTGGCCGGCGAAAGTGCTGGTATCTACAACCTCTGGAGAACAGA  
-----+-----+-----+-----+-----+-----+ 2520  
GGTAAACACCAAGCTCCACCGGCCGCTTTCACGACCATAGATGTTGAGACCTCTTGTCT

a P F V V R G G R R K V L V S T T L E N R -  
2521 AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTTCTCTAGAAACCTCCACCTGGCC  
-----+-----+-----+-----+-----+-----+ 2580  
TTCCTTTTACGAATGTTATGCTCGGACTCATAGTAGAAGAGATCTTTGGAGGTGGACCGG

a K E N A Y N T S L S I I F S R N L H L A -  
2581 AGTCTCACTCCTCAGAGAGAGAGCCCAATAAAGGTGGAATGTGCCGCCCTTCTGCTCAT  
-----+-----+-----+-----+-----+-----+ 2640  
TCAGAGTGAGGAGTCTCTCTCTCGGGTTATTTCCACCTTACACGGCGGGGAAGACGAGTA

a S L T P Q R E S P I K V E C A A P S A H -  
2641 GCCCGGCTCTGCAGTGTGGGGCATCCTGTCTTCCAGACTGGAGCCAAGGTGACCTTTCTG  
-----+-----+-----+-----+-----+-----+ 2700  
CGGGCCGAGACGTCACACCCCGTAGGACAGAAGGTCTGACCTCGGTTCCACTGGAAAGAC

a A R L C S V G H P V F Q T G A K V T F L -  
2701 CTAGAGTTTGAGTTTAGCTGCTCCTCTCTCCTGAGCCAGGTCTTTGGAAGCTGACTGCC  
-----+-----+-----+-----+-----+-----+ 2760  
GATCTCAAACCTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCTTCGACTGACGG

a L E F E F S C S S L L S Q V F G K L T A -  
2761 AGCAGTGACAGCCTGGAGAGAAATGGCACCCTTCAAGAAAACACAGCCAGACCTCAGCC  
-----+-----+-----+-----+-----+-----+ 2820  
TCGTCACTGTCTGGACCTCTCTTTACCGTGGGAAGTTCTTTTGTGTCGGGTCTGGAGTCGG

a S S D S L E R N G T L Q E N T A Q T S A -  
2821 TACATCCAATATGAGCCCCACCTCCTGTTCTCTAGTGAGTCTACCTGCACCGCTATGAG  
-----+-----+-----+-----+-----+-----+ 2880  
ATGTAGGTTATACTCGGGGTGGAGGACAAGAGATCACTCAGATGGGACGTGGCGATACTC

a Y I Q Y E P H L L F S S E S T L H R Y E -  
2881 GTTCACCCATATGGGACCCTCCAGTGGGTCTTGGCCAGAAATCAAAACCACTCTCAGG  
-----+-----+-----+-----+-----+-----+ 2940  
CAAGTGGGTATACCCTGGGAGGGTCACCCAGGACCGGGTCTTAAGTTTTGGTGAGAGTCC

a V H P Y G T L P V G P G P E F K T T L R -  
2941 ACTAACAATGCAAGCTGCATAGTGAGAACCTGACTGAACCCCCAGGCCACCTGTGCAT  
-----+-----+-----+-----+-----+-----+ 3000  
TGATTGTTACGTTTCGACGTATCACGTCTTGGACTGACTTGGGGGTCCGGGTGGACACGTA

a T N N A S C I V Q N L T E P P G P P V H -  
3001 CCAGAGGAGCTTCAACACACAAACAGACTGAATGGGAGCAATACTCACTGTCAAGTGGTG  
-----+-----+-----+-----+-----+-----+ 3060  
GGTCTCCTCGAAGTTGTGTGTTTGTCTGACTTACCCTCGTTATGAGTCACAGTCCACCAC

a P E E L Q H T N R L N G S N T Q C Q V V -  
3061 AGGTGCCACCTTGGGCAGCTGGCAAAGGGGACTGAGGTCTCTGTTGGACTATTGAGGCTG  
-----+-----+-----+-----+-----+-----+ 3120  
TCCACGGTGGAAACCCGTCGACCGTTTCCCTGACTCCAGAGACAACCTGATAACTCCGAC

a R C H L G Q L A K G T E V S V G L L R L -  
GTTCAACAATGAATTTTCCGAAGAGCCAAGTTCAGTCCCTGACGGTGGTCAGCACCTTT  
3121 -----+-----+-----+-----+-----+-----+-----+ 3180  
CAAGTGTTACTTAAAAAGGCTTCTCGGTTCAAGTTCAGGGACTGCCACCAGTCGTGGAAA

a V H N E F F R R A K F K S L T V V S T F -  
GAGCTGGGAACCGAAGAGGGCAGTGTCTACAGCTGACTGAAGCCTCCCGTTGGAGTGAG  
3181 -----+-----+-----+-----+-----+-----+-----+ 3240  
CTCGACCCTTGGCTTCTCCCGTCACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTC

a E L G T E E G S V L Q L T E A S R W S E -  
AGCCTCTTGGAGGTGGTTCAGACCCGGCCTATCCTCATCTCCCTGTGGATCCTCATAGGC  
3241 -----+-----+-----+-----+-----+-----+-----+ 3300  
TCGAGAAACCTCCACCAAGTCTGGCCGGATAGGAGTAGAGGGACACCTAGGAGTATCCG

a S L L E V V Q T R P I L I S L W I L I G -  
AGTGTCTCTGGGAGGGTGTCTCTGCTCTCTCTGTCTTCTGCTGTGGAAGCTTGGC  
3301 -----+-----+-----+-----+-----+-----+-----+ 3360  
TCACAGGACCCTCCCAACGAGGACGACGAGAGGAACAGAAGACGGACACCTTCGAACCG

a S V L G G L L L L A L L V F C L W K L G -  
TTCTTTGCCCATAGAAGAAATCCCTGAGGAAGAAAAAGAGAAGAGAAGTTGGAGCAATGA  
3361 -----+-----+-----+-----+-----+-----+-----+ 3420  
AAGAAACGGGTATTCTTTTAGGGACTCCTTCTTTTCTCTTCTTCAACCTCGTTACT

a F F A H K K I P E E E K R E E K L E Q  
ATGTAGAATAAGGGTCTAGAAAGTCCCTCCCTGGCAGCTTTCTTCAAGAGACTTGCATAAA  
3421 -----+-----+-----+-----+-----+-----+-----+ 3480  
TACATCTTATTCCCAGATCTTTCAGGAGGGACCGTCGAAAGAAGTTCTCTGAACGTATTT

AGCAGAGGTTTGGGGGCTCAGATGGGACAAGAAGCCGCTCTGGACTATCTCCCCAGACC  
3481 -----+-----+-----+-----+-----+-----+-----+ 3540  
TCGTCTCAAACCCCGAGTCTACCCTGTTCTTCGGCGGAGACCTGATAGAGGGGTCTGG

AGCAGCCTGACTTGACTTTTGTAGTCTAGGGATGCTGTGGCTAGAGATGAGGCTTTACC  
3541 -----+-----+-----+-----+-----+-----+-----+ 3600  
TCGTCTGACTGAAGTGAAGTCTAGGATCCCTACGACGACCGATCTCTACTCCGAAATGG

TCAGACAAGAAGAGCTGGCACCAAACTAGCCATGCTCCACCCCTCTGCTTCCCTCCTCC  
3601 -----+-----+-----+-----+-----+-----+-----+ 3660  
AGTCTGTTCTTCTCGACCGTGGTTTTGATCGGTACGAGGGTGGGAGACGAAGGGAGGAGG

TCGTGATCCTGGTTCATAGCCAACTAGGGGCTTTTGTGTTGGGGTCTTTTATCCCCAG  
3661 -----+-----+-----+-----+-----+-----+-----+ 3720  
AGCACTAGGACCAAGGTATCGGTTGTGACCCCGAAAAACAACCCAGGAAATAGGGGTC

GAATCAATAATTTTTTGCCTAGGAAAAAAAAGCGGCCGCGCAATTCGATATCAAGCT  
3721 -----+-----+-----+-----+-----+-----+-----+ 3779  
CTTAGTTATTAAAAAACGGATCCTTTTTTTTTTCGCCGGCGCTTAAGCTATAGTTCGA

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## (2) INFORMATION FOR SEQ ID NO. 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid and amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (iii) MOLECULAR TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) CELLTYPE: chondrocyte

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

NdeI  
|

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GGGGCATATGGTTTCAGAACCTGGGTTGCTACGTTGTTTCCGGTCTGATCATCTCCGCTCT
1 -----+-----+-----+-----+-----+-----+-----+ 60
CCCCGTATACCAAGTCTTGGACCAACGATGCAACAAAGGCCAGACTAGTAGAGGCGAGA

b      G H M V Q N L G C Y V V S G L I I S A L -

GCTGCCGGCTGTTGCTCACGGTGGTAACTACTTCCTAAGCTTGTCCCAGGTTATCAGCGG
61 -----+-----+-----+-----+-----+-----+ 120
CGACGGCCGACAACGAGTGCCACCATTGATGAAGGATTCGAACAGGGTCCAATAGTCGCC

b      L P A V A H G G N Y F L S L S Q V I S G -

BamHI
|
CCTGGTGCCGCGCGGATCCCCC
121 -----+-----+-----+-----+ 143
GGACCACGGCGCGCCTAGGGGGG

b      L V P R G S P -
```